

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Claim 1 (Cancelled).

2 (Previously presented). A method according to claim 25, further comprising amplification of the interacted nucleic acids and quantification of the amplification product.

3 (Previously presented). A method according to claim 25, wherein the binding moiety of the proximity probes is selected from the group consisting of proteins, peptides, carbohydrates, nucleic acids and combinations thereof.

4 (Previously presented). A method according to claim 25, wherein the one or more analytes are selected from the group consisting of proteins, protein aggregates, prions and nucleic acids.

5 (Previously presented). A method according to claim 25, wherein the binding sites for the binding moieties of the proximity probes are on one and the same analyte, or on two close analytes.

6 (Previously presented). A method according to claim 25, wherein the binding moieties are antibodies and said antibodies each bind to the one or more analytes via a further antibody having binding specificity for the one or more analytes analyte(s), and wherein the binding moieties are directed against the Fc portion of the further antibody.

7 (Previously presented). A method according to claim 25, wherein the interaction of said nucleic acids

coupled to the binding moieties is through hybridisation to a common splint template and ligation of the nucleic acid ends.

Claims 8-12 (Cancelled).

13 (Previously presented). A method according to claim 25 for screening for ligand-receptor interaction antagonists in a high throughput screening procedure, wherein a drug candidate molecule is screened for ability to disrupt proximity between the proximity probes.

14 (Previously presented). A method according to claim 25, wherein the first proximity probe comprises a purified analyte coupled to an oligonucleotide and the second proximity probe comprises a binding moiety specific for the analyte and coupled to an oligonucleotide which interacts with the oligonucleotide of the first proximity probe if the first and second proximity probes are in close proximity.

15 (Previously presented). A method according to claim 25, further comprising screening a drug candidate molecule, which is a biomolecule derived from a library of potential ligands, for the ability to disrupt proximity between the proximity probes by binding to one of the binding sites involved in the formation of the proximity between the proximity probes.

Claim 16 (Cancelled).

17 (Previously presented). A method according to claim 25, comprising using said method for the detection of infectious agents.

18 (Previously presented). A method according to claim 17, wherein the infectious agents are detected in food for humans and animals.

19 (Previously presented). The method according to claim 25, further comprising quantifying the interaction of the analytes in solution.

20 (Previously presented). A method according to claim 19, further comprising amplification of the interacted nucleic acids and quantification of the amplification product.

21 (Previously presented). A method according to claim 14, wherein the presence of an analyte in a sample is detected as a decrease in signal.

22 (Previously presented). A method according to claim 25, wherein said two or more proximity probes comprise a first said proximity probe with a 3' free nucleic acid (A), a second said proximity probe with a 5' free nucleic acid (B), and a third said proximity probe with both 3' and 5' free nucleic acids (C), and wherein the 3' end of A interacts with the 5' end of C and the 3' end of C interacts with the 5' end of B.

23 (Previously presented). A method according to claim 3, wherein the proteins are selected from the group consisting of monoclonal antibodies, polyclonal antibodies, lectins, soluble cell surface receptors, combinatorially derived proteins from phage display, and combinatorially derived proteins from ribosome display.

24 (Previously presented). The method of claim 3,
wherein the nucleic acids are aptamers.

25 (Previously presented). A method for detecting
the presence of one or more analytes in solution, comprising:

a) binding two or more proximity probes to a
respective binding site on said one or more analytes not
immobilized on a solid support,

wherein each proximity probe comprises a binding
moiety with affinity for said one or more analytes and nucleic
acids acting as a reactive functionality coupled to the
binding moiety;

b) allowing the binding moiety to bind to the one or
more analytes other than by Watson-Crick base pairing and
allowing the nucleic acids of the proximity probes to interact
with each other if the proximity probes are in close proximity
to each other; and

c) detecting the degree of interaction between the
nucleic acids, thereby detecting the presence of one or more
analytes in solution.

26 (Previously presented). The method of claim 25,
wherein the one or more analytes are selected from the group
consisting of proteins, protein aggregates, and prions.

27 (Previously presented). The method of claim 25,
wherein the one or more analytes are not nucleic acids.

28 (New). A method for detecting one or more
analytes in solution, comprising:

- a) binding two or more proximity probes to a respective binding site on said one or more analytes not immobilized on a solid support,
 - wherein the proximity probes comprise a binding moiety with affinity for said one or more analytes and nucleic acids acting as a reactive functionality coupled thereto;
- b) allowing the binding moiety to bind to the one or more analytes other than by Watson-Crick base pairing and allowing the nucleic acids to interact with each other if they are in close proximity to each other; and
- c) detecting the degree of interaction between the nucleic acids.